

R. Shukla

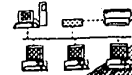
**RAW SEQUENCE LISTING**  
**ERROR REPORT**

RECEIVED

APR 30 2001

TECH CENTER 1600/2900

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



5-1-01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/465,978  
Source: 1632  
Date Processed by STIC: 4-17-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/465, 978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**
- 10 ☒ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
**Please explain source of genetic material in <220> to <223> section.**  
**(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)**
- 13 ☐ PatentIn ver. 2.0 "bug"      **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1632

RAW SEQUENCE LISTING                      DATE: 04/17/2001  
 PATENT APPLICATION: US/09/465,978              TIME: 13:03:13

Input Set : A:\PXE-012.US seqlist.txt  
 Output Set: N:\CRF3\04172001\I465978.raw

3 <110> APPLICANT: Zhang, Ning and Anthony Purchio  
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ANGIOGENESIS  
 6        MODULATING COMPOUNDS  
 8 <130> FILE REFERENCE: PXE-012.US  
 10 <140> CURRENT APPLICATION NUMBER: US/09/465,978  
 11 <141> CURRENT FILING DATE: 1999-12-16  
 13 <150> PRIOR APPLICATION NUMBER: 60/152,522  
 14 <151> PRIOR FILING DATE: 1999-09-03  
 16 <160> NUMBER OF SEQ ID NOS: 51  
 18 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply  
 Corrected Diskette Needed  
 See pp. 1-2-4

# ERRORED SEQUENCES

531 <210> SEQ ID NO: 40  
 532 <211> LENGTH: 7093  
 533 <212> TYPE: DNA  
 534 <213> ORGANISM: Mus sp.  
 536 <400> SEQUENCE: 40  
 537 ggtaccaaag catagaacta cagatccgct ctctgcctgt accaccctct ggcatttaat 60  
 538 cacacaatgc ttggttttgt tottcaactt ttctgttat gatgcagtc ctggcttg 120  
 539 taactatgag ctccaagc aaagaacgca tcatctattt ttgtgtctct tctccaagg 180  
 540 acttagtgta tcacttactg gctaaatgct tgagacaaaa acagggatta atgaagaaga 240  
 541 aagagaaaaga aaagggaagg aaagtgccca caattactga cagggtttca gtaaagcagt 300  
 542 ctaggagggtc aggtattttc catagccatg cccagagtg ggtgttgcca cttagctgc 360  
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 544 tgtaagtac tgcagattta cagaaagcct catggagggtc tgtaagaagc cagagggtat 480  
 545 aacaccaaga tttagagcca ctgaccagca gaatgcagaa tgtccaggct atgatccagg 540  
 546 ttgtagatcc tgatctgact actcaagact gggtgaaggc aaggttcact tggattcact 600  
 547 ctatttgcca gcagatgttt taaatccatc atatataat atatctctc attactttag 660  
 548 gacagtgttt ctgagccttc ctaatgctgt agccctttaa tagagttcct catattgtga 720  
 549 ttgtaaaaat tattttgttg ctacttcatg actaattttg ctactgtgaa agggtcattt 780  
 550 taccgccaggc tgttgagacc cacatgttgg gaaccactac tttagaaggc attggggttg 840  
 551 gagaagaaca tgaagaatag agtaacagtg gtcagttttg gttcattata tcacagaaac 900  
 552 attcacttta aggtttcagc atgtttgttg tgtatatgtg attgtgtaa gacttcacca 960  
 553 ggtctttctt taatcaccat acctaacatc ttaccactc catatccatc agcttcacct 1020  
 554 tgactctag catttgggca ttcactcctgt accagggcag gcatccatc ttttgcaact 1080  
 555 cacattgttt ctagtttttg attattacca acaatgttc tagaccatga attttgtct 1140  
 556 ttgacttttg ctttgtaaac atcataaaac aatccagtgg tgggtgtgtg gccgtgctg 1200  
 557 ctgggtgtgg ttgtaaaagca ggaagccata aagtgccttt attcaatctg tatttgatac 1260  
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 563 ttgaaaatg ccacaatgaa acctaattta caaaagaacc actatatgac cttcacagtg 1620  
 564 tgtgctaagt cttggagatt tagtggtgaa gaagtcaggt gtgtttccaa tctcatggag 1680

Missing mandatory <220> to <223> features  
 to explain the "n" at position 3617 in  
 Seq. #40. (See next page)

Also see #10  
 on the Error  
 Summary Sheet.

## RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:13

Input Set : A:\PXE-012.US seqlist.txt

Output Set: N:\CRF3\04172001\I465978.raw

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567 gtggtcttca aagacccttt agaagctgag aactaaagac agcaagcaag gtgagggcag 1860
568 catctccacc tttccagtgg aatgagcaac ttagggtata cagctgattc ccacattgtc 1920
569 aacaaggctc ttcagagact agagatgcac taatgatgac catacccagc ttttaaggaa 1980
570 ggtttctgag catgtccaag caccctacac taggcattgg aaatcaacat gtccagagat 2040
571 ggaagtgaca gtcagtaagc caaccctttt caaaaacttc aaagctatta ctctgcaact 2100
572 ctccagacat attggccccc agtgtgttgg gaagctctca ttattgttct ttgattgggt 2160
573 ctctacattc cgagatccaa ggagcagtta tctcaggtag aggatcgtgg aatgtctgcc 2220
574 catgattaac ttcaatttat acctgtaagt tataccacat cctaaacacg ctgatgtccc 2280
575 agagaacatt ttgaccagct gctaacaaaa ccaggagca tttagaaaaa aactgagtca 2340
576 cccaccgttc tggataatga tggagagaaa caaatgggat tattcttaca gagtatgaaa 2400
577 gttacataat ttctctggat aatggagaat taattaaaca tcagcatctt ttctggactg 2460
578 cagaggggaag acagaggtga agccaatctt tccgggaaat ggaggaggaa agaatttgac 2520
579 tactatttgg gggttaacaa tacatcttac tagcatggca aaggaaactg ggctgctttt 2580
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582 caaaaaatccc aggccagctt agtttgtgta acaagacctt tgctcaaaac aagatttaca 2760
583 aaacaaacaa gcaacaaaaa aaatataaaa aaggagaaga aaataactgc cagggggaggc 2820
584 tgtgagcaat gaagacttga tgagtgaaca tctcgcacag tggacgcttg tgtctagaag 2880
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586 tggacttcac aatgtctcag ctccagggtc tttatacaga gcatattagc cacatgtggt 3000
587 agcttgtgcc tghtaatgtg gcacttgaga gaccaagaca ggaggattgc cacaagtctc 3060
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595 cccgccccca cccaacacct gatcctgccc cctttctctc ccccttctct ctctaaacca 3540
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E--> 597 gcatcctcac ttggacttcc cttcttgtta aacttcatat ggtctgtgag ttgtatcatg 3660
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```

→ see p.1  
 explanation.

## RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:13

Input Set : A:\PXE-012.US seqlist.txt

Output Set: N:\CRF3\04172001\I465978.raw

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654 gtgagttggt gaaagcttcc cagggaacta tgcctcatctg tggacgctg atggggagat 7080
655 ctggggaagt atg 7093

```

09/465, 978  
End of  
Seg. #51 (partially shown)

p. 4

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ttactagagc tcagtt 11176
```

PXE-012.US

2

→ Delete extraneous material from  
the end of the file. It is causing  
a program error.

## VERIFICATION SUMMARY

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:14

Input Set : A:\PXE-012.US seqlist.txt

Output Set: N:\CRF3\04172001\I465978.raw

L:597 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40  
L:1066 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:1068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:51